

Figure 1

1 RTPSDKPVAH VVANPQAEGQ LQWLNRRAA LLANGVELRD NQVVVPSEGQ
51 YLIYSQVLFK GQGCPSTHVL LTHTISRIAV SYQTKVNLLS AIKSPCQRET
101 PEGAEAKPWF EPIYLGGVFQ LEKGDRILSAE INRPDYLFA ESGQVYFGII
151 AL (SEQ ID NO: 6)

Figure 2

1 HSDPARRGQL SVCDSISEWV TAADKKTAVD MSGGTVTVLE KVPVSKGQLK
51 QFYETKCNP MGYTKEGCRG IDKRWNSQC RTTQSYVRAL TMDSKRIGW
101 RFIRIDTSCV CTLTIKRGR (SEQ ID NO: 7)

FIGURE 3

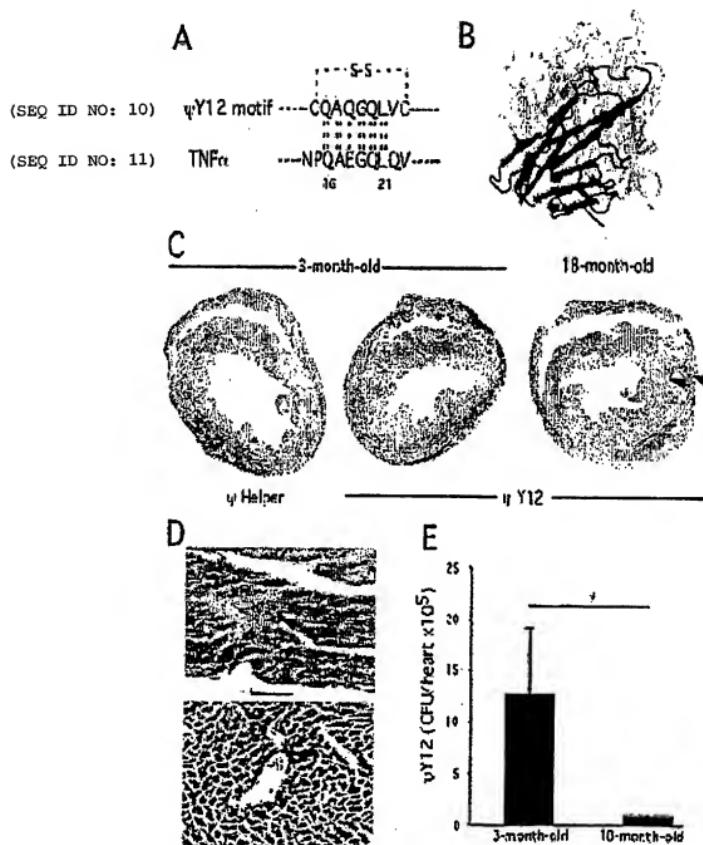


FIGURE 6

